

Query Match 76.7%; Score 2052.5; DB 1; Length 418;
 Best Local Similarity 97.8%; Pred. No. 5.7e-130;
 Matches 399; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 96 GMCCKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTEFNKIPNLAEFAFSLYROLAHOSN 155
 DB 14 GLC---CLVPVSLAEDPQGDAAQKTDTSHHDQDHPTEFNKIPNLAEFAFSLYROLAHOSN 70

QY 156 STNIFSPVSIATAFAMLSLGTADTHDEILGLNPNLTPTEPAQIHGEGFQELLRLNQP 215
 DB 71 STNIFSPVSIATAFAMLSLGTADTHDEILGLNPNLTPTEPAQIHGEGFQELLRLNQP 130

QY 216 DSOLQLTGNGFLSEGLKLVDFKLEDAKLYHSEAFVNFCDTEAKKQINDYVEKGTQ 275
 DB 131 DSOLQLTGNGFLSEGLKLVDFKLEDAKLYHSEAFVNFCDTEAKKQINDYVEKGTQ 190

QY 276 GKIVDLVKELDRDTVFALVNYIFFKQKWERPEVKDTEEDPHVDQVTVTKVPMKRLGM 335
 DB 191 GKIVDLVKELDRDTVFALVNYIFFKQKWERPEVKDTEEDPHVDQVTVTKVPMKRLGM 250

QY 336 FNIOHCKKLSWVLLMKYLGNTATAFFLPDEGKLOHLENLTHDIITKFLNEDRRSASL 395
 DB 251 FNIOHCKKLSWVLLMKYLGNTATAFFLPDEGKLOHLENLTHDIITKFLNEDRRSASL 310

QY 396 HLPKLSITGYDLKSVLGOLGITKVFSGNADLSGVTEAPLKLKAVHKAVLTIDEKGT 455
 DB 311 HLPKLSITGYDLKSVLGOLGITKVFSGNADLSGVTEAPLKLKAVHKAVLTIDEKGT 370

QY 456 AGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPFLMGKVVNPTQK 503
 DB 371 AGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPFLMGKVVNPTQK 418

RESULT 2

ALAT_PAPAN STANDARD; PRT; 409 AA.

AC P01010;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
 DE antiprotease) (AAT) (Fragment).
 GN SERPINAL OR PI.
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Papio.
 OX NCBI_TaxID=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82082539; PubMed=7031661;
 RA Kurachi K., Chandra T., Friesner Degen S.J., White T.T.,
 RA Marchioro T.B., Woo S.L.C., Davie E.W.;
 RT "Cloning and sequence of cDNA coding for alpha 1-antitrypsin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:6826-6830(1981).
 CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS
 CC ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
 CC THROMBIN.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC ENBL; J00321; AAA35377.1; -
 DR PIR; A01248; ITBA.

DR HSSP; P01009; 9API.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 15
 FT CHAIN 16 409
 FT ACT_SITE 373 374
 FT CARBOHYD 61 61
 FT CARBOHYD 98 98
 FT CARBOHYD 136 136
 FT CARBOHYD 262 262
 SQ SEQUENCE 409 AA; 45694 MW; E19B0B7450FDBA9B CRC64;

Query Match 71.4%; Score 1909.5; DB 1; Length 409;
 Best Local Similarity 90.2%; Pred. No. 2e-120;
 Matches 368; Conservative 21; Mismatches 16; Indels 3; Gaps 1;

QY 96 GMCCKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTEFNKIPNLAEFAFSLYROLAHOSN 155
 DB 5 GLC---CLLPGLSLAEDPQGDAAQKTDTPHDQNHFTLNKIPSLAEFAFSLYROLAHOSN 61

QY 156 STNIFSPVSIATAFAMLSLGTADTHDEILGLNPNLTPTEPAQIHGEGFQELLRLNQP 215
 DB 62 STNIFSPVSIATAFAMLSLGTADTHDEILGLNPNLTPTEPAQIHGEGFQELLRLNKP 121

QY 216 DSOLQLTGNGFLSEGLKLVDFKLEDAKLYHSEAFVNFCDTEAKKQINDYVEKGTQ 275
 DB 122 DSOLQLTGNGFLSEGLKLVDFKLEDAKLYHSEAFVNFCDTEAKKQINDYVEKGTQ 181

QY 276 GKIVDLVKELDRDTVFALVNYIFFKQKWERPEVKDTEEDPHVDQVTVTKVPMKRLGM 335
 DB 182 GKIVDLVKELDRDTVFALVNYIFFKQKWERPEVKDTEEDPHVDQVTVTKVPMKRLGM 241

QY 336 FNIOHCKKLSWVLLMKYLGNTATAFFLPDEGKLOHLENLTHDIITKFLNEDRRSASL 395
 DB 242 FNIOHCKKLSWVLLMKYLGNTATAFFLPDEGKLOHLENLTHDIITKFLNENRRSASL 301

QY 396 HLPKLSITGYDLKSVLGOLGITKVFSGNADLSGVTEAPLKLKAVHKAVLTIDEKGT 455
 DB 302 HLPKLSITGYDLKSVLGOLGITKVFSGNADLSGVTEAPLKLKAVHKAVLTIDEKGT 361

QY 456 AGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPFLMGKVVNPTQK 503
 DB 362 AGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPFLMGKVVNPTQK 409

RESULT 3

ALAT_PIG STANDARD; PRT; 421 AA.

AC P50447;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
 DE antiprotease).
 GN SERPINAL OR PI.
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=97009792; PubMed=8856896;
 RA Archibald A.L., Couperwhite S., Mellink C.H.M., Lahbib-Mansais Y.,
 RA Gellin J.;
 RT "Porcine alpha-1-antitrypsin (PI): cDNA sequence, polymorphism and
 RT assignment to chromosome 7q2.4-q2.6";
 RL Anim. Genet. 27:85-89(1996).
 CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS

Mon Dec 9 12:51:04 2002

CC ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
CC THROMBIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC -----
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CC -----
CC EMBL; X88780; CAA61259.1; -
CC HSP: P01009; 9API.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
CC FT SIGNAL 1 24
CC FT CHAIN 25 421
CC FT ACT_SITE 385 386
CC FT CARBOHYD 73 73
CC FT CARBOHYD 110 110
CC FT CARBOHYD 421 AA; 47194 MW; 08A4AB2A9E600690 CRC64;
CC SEQUENCE 421 AA; 47194 MW; 08A4AB2A9E600690 CRC64;
CC -----
CC Query Match 56.4%; Score 1508; DB 1; Length 421;
CC Best Local Similarity 72.0%; Pred. No. 1.3e-93;
CC Matches 296; Conservative 40; Mismatches 69; Indels 6; Gaps 2;

QY 96 GMGKSCVSPVKAMEDPQGDAAQKDTSHDQD---HPTFNKITPNLAFAFSLYRQLAH 152
DB 14 GLC---CLVPISLAEGIQGHAVQETDVPDRHDEHQEAACHRIAPNLADFAFSLYRQVAR 70
QY 153 QSNSTNFFSPVSIATAFAMLSLGTADHDEILEGLNLFNLTPEAQIHGEGFQELLRTL 212
DB 71 QSNSTNFFSPVSIATAFAMLSLGTADHDEILEGLNLFNLTPEAQIHGEGFQELLRTL 130
QY 213 NQPSQQLTNGFLSEGLKLVKDFLEDDVKLYHSEAFVNFVGTETEAQKQINDYVEK 272
DB 131 NQPSQQLTNGFLSEGLKLVKDFLEDDVKLYHSEAFVNFVGTETEAQKQINDYVEK 190
QY 273 GTQKIVDLVKELDRVTFALVNYIFFKQKWERPFVEKDEEDFHVDTTVKVPMMKR 332
DB 191 GSQKIVDLVDELKDTVFALVNYIFFKQKWERPFVEKDEEDFHVDTTVKVPMMNR 250
QY 333 LGMFNIQKCKLSSWLLMKYLGATATFFLPDQGLKQHLNLTHTDITKFLNEDRRS 392
DB 251 LGMFNIQKCKLSSWLLMKYLGATATFFLPDQGLKQHLNLTHTDITKFLNEDRRS 310
QY 393 ASLHLPKLSITGYDLKSVLGQGLTKVFSNGADLSGVTEAPLKLKSKAVHKAVLTIDEK 452
DB 311 ANLHLPKLSITGYDLKSVLGQGLTKVFSNGADLSGVTEAPLKLKSKAVHKAVLTIDEK 370
QY 453 GTEAAGMFLAIPMSIPPEVKFNKPFVFLMEQNTKSPFPMGVNPTQ 503
DB 371 GTEAAGMFLAIPMSIPPEVKFNKPFVFLMEQNTKSPFPMGVNPTQ 421

RESULT 4
ALAT_CALCN STANDARD; PRG: 412 AA.
AC 054763;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-1-antitrypsin precursor (Alpha-1-antitrypsin) (Alpha-1-
DE proteinase inhibitor).
OS Callosciurus caniceps (Gray-bellied squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scluridae; Sciurinae;
OC Callosciurus.

NCBI_TaxID=64664;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=98094263; PubMed=9434174;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RT Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RT "Expression of multiple alaphal-antitrypsin-like genes in hibernating
RT species of the squirrel family.";
RL Gene 204:127-132(1997).
CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES (By similarity).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC -----
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CC -----
CC EMBL; AB000552; BAA24422.1; -
CC HSP: P01009; 9API.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
CC FT SIGNAL 1 24
CC FT CHAIN 25 412
CC FT ACT_SITE 377 378
CC FT CARBOHYD 65 65
CC FT CARBOHYD 102 102
CC FT CARBOHYD 165 165
CC FT CARBOHYD 266 266
CC FT CARBOHYD 412 AA; 45729 MW; 7235668E9E8FCC6 CRC64;
CC SEQUENCE 412 AA; 45729 MW; 7235668E9E8FCC6 CRC64;
CC -----
CC Query Match 56.1%; Score 1500; DB 1; Length 412;
CC Best Local Similarity 71.0%; Pred. No. 4.4e-93;
CC Matches 289; Conservative 48; Mismatches 62; Indels 8; Gaps 2;

QY 96 GMGKSCVSPVKAMEDPQGDAAQKDTSHDQDHPFTFNKITPNLAFAFSLYRQLAHOSN 155
DB 14 GLC---CLAPGSLAGD---AQETDASKDDHEHPACHAPNLAEFAFDLYRVLARQSN 65
QY 156 STNIFSPVSIATAFAMLSLGTADHDEILEGLNLFNLTPEAQIHGEGFQELLRLNOP 215
DB 66 TTNIFSPVSIATAFAMLSLGTADHDEILEGLNLFNLTPEAQIHGEGFQELLRLNOP 125
QY 216 DSQQLTNGFLSEGLKLVKDFLEDDVKLYHSEAFVNFVGTETEAQKQINDYVEKGTQ 275
DB 126 NNQQLTNGFLSEGLKLVKDFLEDDVKLYHSEAFVNFVGTETEAQKQINDYVEKGTQ 185
QY 276 GKIVDLVKELDRDTVFALVNYIFFKQKWERPFVEKDEEDFHVDTTVKVPMMKRLGM 335
DB 186 GKIVDLVKELDRDTVFALVNYIFFKQKWERPFVEKDEEDFHVDTTVKVPMMKRLGM 245
QY 336 FNIQKCKLSSWLLMKYLGATATFFLPDQGLKQHLNLTHTDITKFLNEDRRSASL 395
DB 246 FDLLYCTTASWVLMQDYLGATATFFLPDQGLKQHLNLTHTDITKFLNEDRRSASL 305
QY 396 HLPKLSITGYDLKSVLGQGLTKVFSNGADLSGVTEAPLKLKSKAVHKAVLTIDEKGT 455
DB 306 YFPKLSITGYDLKSVLGQGLTKVFSNGADLSGVTEAPLKLKSKAVHKAVLTIDEKGT 365
QY 456 AAGAMFLAIPMSIPPEVKFNKPFVFLMEQNTKSPFPMGVNPTQ 502
DB 366 AAGVTVLEAIPMSIPPEVKFNKPFVFLMEQNTKSPFPMGVNPTQ 412

RESULT 5

[illegible]

RT "Expression of multiple alpha-antitrypsin-like genes in hibernating
species of the squirrel family."
RL Gene 204:127-132(1997).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
CC ANTITRYPSIN.
CC
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CC
CC EMBL: AB000546; BAA24416.1; -
CC HSP: P01009; BAPI.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF000079; serpin; 1.
CC SMART: SM00093; SERPIN; 1.
CC PROSITE: PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Signal.
KW SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 413 ALPHA-1-ANTITRYPSIN-LIKE PROTEIN CM55-MM.
FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).
FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 413 AA; 48212 MW; D1C37B899BB20B69 CRC64;

Query Match 54.1%; Score 1447.5; DB 1; Length 413;
Best Local Similarity 68.3%; Pred. No. 1.4e-89;
Matches 274; Conservative 60; Mismatches 62; Indels 5; Gaps 1;

QY 101 SCVSPVAMEPQDGAQKDTSHDDQDHTFNKNTPLNAEFAFSLYROLAHQSNSTNIF 160
DB 16 SCLGPGSLAQD-----AQETASKKDQEHASHRIAPLAEFALSFLYRLAHQSNSTNIF 70
QY 161 PSPSIATAFAMLSLGTADTHDEILGLNFNLTEPEAQIHGFEQLLTLNQPSQLQ 220
DB 71 PSPSIATAFAMLSLGTADTHDEILGLNFNLTEPEAQIHGFEQLLTLNQPSQLQ 130
QY 221 LTTGNGLFLSEGLKLVDFLEDKVLYHSEAFVNFQDTEAKKQINDYVEKGTQGIKD 280
DB 131 LTTGNGLFIHQNLKLLDKFLEDKVLYHSEALPTNFTEARQQINSYVEKGTQGIKE 190
QY 281 LVKELDRDTVFALVNIFFKQKWERPEVKDTEEDFHVQDVTTVPMKRLGMFNIQH 340
DB 191 LVKELDRDTVFALVNIFFKQKWERPEVKDTEEDFHVQDVTTVPMKRLGMFNIQH 250
QY 341 CKKLSWLLMKYLGNAFAIFLPPDEGLKQHLNETHLTHDITKFELEDRRSASLHPLK 400
DB 251 CSTLASWLVQMDYLGNAFAIFLPPDKGKQHLNETHLTHDITKFELEDRRSASLHPLK 310
QY 401 SITGYDLKSVLGOLGITKVFSGADLSGVTEAPKLKSAVHKAVLTIDKGTGAAGAM 460
DB 311 SISGTYDLKSVLGOLGITKVFSGADLSGVTEAPKLKSAVHKAVLTIDKGTGAAGAM 370

RESULT 8
ALAT_BOVIN STANDARD; PRT; 416 AA.
ID ALAT_BOVIN
AC P34955;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Alpha-1-antitrypsin precursor (Alpha-1-antitrypsin) (Alpha-1-

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CC EMBL: X15555; CAA33561.1; -
CC PIR: S05312; ITSH.
CC HSP: P01009; 1KCT.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF000079; serpin; 1.
CC SMART: SM00093; SERPIN; 1.
CC PROSITE: PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
KW SIGNAL 1 24 ALPHA-1-ANTITRYPSIN-LIKE PROTEIN CM55-MM.
FT CHAIN 25 416 REACTIVE BOND.
FT ACT_SITE 380 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 39 39 A -> S (IN REF. 2).
FT CONFLICT 45 45 C -> A (IN REF. 2).
SQ SEQUENCE 416 AA; 45984 MW; 0B4702C0527321BF CRC64;

Query Match 54.8%; Score 1465.5; DB 1; Length 416;
Best Local Similarity 67.8%; Pred. No. 8.9e-91;
Matches 280; Conservative 62; Mismatches 67; Indels 5; Gaps 2;

QY 89 RDLKCCMGCKSCVSPVAMEPQDGAQKDTSHDDQDHTFNKNTPLNAEFAFSLYR 148
DB 7 RGLLLAALC---CLAPTSAGVLQGHAVQETDTHAQE--AACHKIAPLANFAFSIYH 61
QY 149 QLAHOSNTNIFPSPVSIATAFAMLSLGTADTHDEILGLNFNLTEPEAQIHGFEQL 208
DB 62 KLAHOSNTNIFPSPVSIATAFAMLSLGTADTHDEILGLNFNLTEPEAQIHGFEQL 121
QY 209 LRTLNQPSQLQTLTGNGFLSEGLKLVDFLEDKVLYHSEAFVNFQDTEAKKQIND 268
DB 122 LRTLNQPSQLQTLTGNGFLSEGLKLVDFLEDKVLYHSEAFVNFQDTEAKKQIND 181
QY 269 YVEKGTQGIKLVDFLEDKVLYHSEAFVNFQDTEAKKQINDYVEKGTQGIKLVDF 328
DB 182 YVEKGTQGIKLVDFLEDKVLYHSEAFVNFQDTEAKKQINDYVEKGTQGIKLVDF 241
QY 329 MKKRLGMFNIQHCKKLSWLLMKYLGNAFAIFLPPDEGLKQHLNETHLTHDITKFE 388
DB 242 MNRLGMFNIQHCKKLSWLLMKYLGNAFAIFLPPDEGLKQHLNETHLTHDITKFE 301
QY 389 DRRSASLHPLKSLTGTVDKSVLGOLGITKVFSGADLSGVTEAPKLKSAVHKAVLT 448
DB 302 YASSANLHPLKSLTGTVDKSVLGOLGITKVFSGADLSGVTEAPKLKSAVHKAVLT 361
QY 449 IDEKGTGAAGAMFLEAIPMSIPPEVKENKPFVFLMIEONTKSPFLMGKVVNPTQ 502
DB 362 IDEKGTGAAGAMFLEAIPMSIPPEVKENKPFVFLMIEONTKSPFLMGKVVNPTQ 415

RESULT 7
ALMM_TAMSI STANDARD; PRT; 413 AA.
ID ALMM_TAMSI
AC O54757;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alpha-1-antitrypsin-like protein CM55-MM precursor.
OS Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Tamias.
ON NCBI_TaxID=64680;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=98094263; PubMed=9434174;
RC Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;

DE protease inhibitor).

GN PI.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=92223096; PubMed=1562597;

RA Sinha D., Bakshi M.R., Kirby E.P.;

RT "Complete cDNA sequence of bovine alpha 1-antitrypsin.";

RL Biochim. Biophys. Acta 1130:209-212(1992).

CC -!- SUBCELLULAR LOCATION: Extracellular.

CC -!- TISSUE SPECIFICITY: PLASMA.

CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

CC -----

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CC -----

DR EMBL; X63129; CAA44840.1; -.

DR PIR; S21097; S21097.

DR PIR; S18920; S18920.

DR HSSP; P01009; 1QIP.

DR InterPro; IPR000215; Serpin.

DR Pfam; PF00079; serpin; 1.

DR SMART; SM00093; SERPIN; 1.

DR PROSITE; PS00284; SERPIN; 1.

KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.

FT SIGNAL 1 24 BY SIMILARITY.

FT CHAIN 25 416 ALPHA-1-ANTITRYPSIN.

FT ACT_SITE 380 381 REACTIVE BOND.

FT CARBOHYD 68 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).

FT SEQUENCE 416 AA; 46104 MW; 3280CDAF42DA35E2 CRC64;

Query Match 54.1%; Score 1447.5; DB 1; Length 416;

Best Local Similarity 56.9%; Pred. No. 1.4e-89;

Matches 277; Conservative 62; Mismatches 70; Indels 5; Gaps 2;

QY 89 RDLCCMGCKGKSCVSPVKAMEDPQDAAOKTDTSHDDQDHPFNKIPNLAFAFSLYR 148

DB 7 RGLLLAALC--CLAPISLAGVLGHVAVQETDTSRQE--AACHKIAPNLANFAFSYH 61

QY 149 QLAHQSNTHIFSPVSIATAFAMLSLGTAKADTHDEILGLNFTLPEAQIHGFGQEL 208

DB 62 HLAHQSNTHIFSPVSIATAFAMLSLGTAKADTHDEILGLNFTLPEAQIHGFGQEL 121

QY 209 LRTLNQDPSQLQTLTNGFLSLGLVDKFLDYKLYHSAFTVNGDTEAAKQIND 268

DB 122 LHTLNQPNHQQLTNGFLSLGLVDKFLDYKLYHSAFTVNGDTEAAKQIND 181

QY 269 YVEKGQTKVDLVKELDRDTPFALVNYIFFKQKWERPPEVKGTEEDFHVQDVTKVP 328

DB 182 YVEKSGHGKIVELVKVLDNPTFALVNYISFKGKWEKPEMKHTTERFHVDEQTKVP 241

QY 329 MKRLGHNFOHQCKLSSVLLMKYLGNTATIFFLPDEKQLHNLTHDITKFLNE 388

DB 242 MMRNLGFDLHYCDKLSASVLLDYGVNVTACFILPDGLKQLEKLNELAKFLKK 301

QY 389 DRRSASLHLPKLSITDYDLKSVLGQGTGKVFNSGADLSGVTEAPKLSKAVHAKVT 448

DB 302 YASSANLHLPKLSISDYDLKSVLGQGTGKVFNSGADLSGVTEAPKLSKAVHAKVT 361

QY 449 IDEKGTAAAGFLEAIPMSIPPEVKFNKPFVFLMEQNTKSPFLFMGVKNPTQ 502

Db 362 IDEKGTAVGSGTFLEAIPMSLPPDVEFNRPFLCILYDRNTPSKPLFVGKVNPTQ 415

RESULT 9

ALST_TAMSI

ID ALST_TAMSI STANDARD; PRT; 413 AA.

AC O54759;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alpha-1-antitrypsin-like protein CM55-ST precursor.

OS Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Tamias.

OX NCBI_TaxID=64680;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=98094263; PubMed=9434174;

RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,

RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;

RT "Expression of multiple alpha1-antitrypsin-like genes in hibernating

RT species of the squirrel family.";

RL Gene 204:127-132(1997).

CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.

CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-

CC ANTITRYPSIN.

CC -----

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CC -----

DR EMBL; AB000548; BAA24418.1; -.

DR HSSP; P01009; 9API.

DR InterPro; IPR000215; Serpin.

DR Pfam; PF00079; serpin; 1.

DR SMART; SM00093; SERPIN; 1.

DR PROSITE; PS00284; SERPIN; 1.

KW Serpin; Serine protease inhibitor; Glycoprotein; Signal.

FT SIGNAL 1 24 POTENTIAL.

FT CHAIN 25 413 ALPHA-1-ANTITRYPSIN-LIKE PROTEIN CM55-ST.

FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).

FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).

FT SEQUENCE 413 AA; 46151 MW; 7A04BFD5C520A55A CRC64;

Query Match 52.5%; Score 1403.5; DB 1; Length 413;

Best Local Similarity 66.5%; Pred. No. 1.2e-86;

Matches 268; Conservative 61; Mismatches 69; Indels 5; Gaps 1;

QY 101 SCVSPVKAMEDPQDAAOKTDTSHDDQDHPFNKIPNLAFAFSLYRQAHQSNTHIF 160

DB 16 SCVSPVKAMEDPQDAAOKTDTSHDDQDHPFNKIPNLAFAFSLYRQAHQSNTHIF 70

QY 161 FSPVSTATFAMLSLGTAKADTHDEILGLNFTLPEAQIHGFGQELRLNPDLSQ 220

DB 71 FSPVSTATFAMLSLGTAKADTHDEILGLNFTLPEAQIHGFGQELRLNPDLSQ 130

QY 221 LTTNGFLSLGLVDKFLDYKLYHSAFTVNGDTEAAKQINDYVEKGTGKIVD 280

DB 131 LTTNGFLSLGLVDKFLDYKLYHSAFTVNGDTEAAKQINDYVEKGTGKIVD 190

QY 281 LYKELDRDTPFALVNYIFFKQKWERPPEVKGTEEDFHVQDVTKVPKMKRLGNFTQH 340

Mon Dec 9 12:51:04 2002

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Db 191 LKELDRDVTALVNYIFFKGGKWKQPNNEQTRKDFHVDVETVVRVPMNRLGMFLHH 250
QY 341 CKKLSSWLLMKYLGKATAIFFLPDEGKQLHLENELTHDIITKFLNEDRRSASLHLPKL 400
Db 251 CSTLASWQLMDYLGKATAIFFLPDEGKQLHLENELTHDIITKFLNEDRRSASLHLPKL 310
QY 401 SITGTYDLKSVLGQGITKVFSGNADLSGVTEAPLKLKAVHKAVLTIDEKGTAAAGM 460
Db 311 SISGTYDLKSVLGQGITKVFSGNADLSGVTEAPLKLKAVHKAVLTIDEKGTAAAGM 370
QY 461 FLEAIPMSIPPEVKFKPFVFLMEQNTKSPLEFMGVNPTOK 503
Db 371 VLGNIRSLRYEIVDRPFLVVIYEHHTKSPLEFMGVNPTOK 413

RESULT 10
ALMS_TAMSI STANDARD; PRT; 413 AA.
ID ALMS_TAMSI STANDARD; PRT; 413 AA.
AC O54760;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Alpha-1-antitrypsin-like protein CM55-SI precursor.
OS Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Tamias.
OX NCBI_TaxID=64680;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98094263; PubMed=9434174;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RA "Expression of multiple alphas-1-antitrypsin-like genes in hibernating
RT species of the squirrel family."
RL Gene 204:127-132(1997).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
CC ANTI-TRYPSIN.
CC
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CC
CC EMBL; AB000549; BAA24419.1; -.
CC HSP; P01009; 9A1.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Signal.
CC SIGNAL 1 24
CC CHAIN 25 413
CC MOD_RES 65 65
CC CARBOHYD 102 102
CC CARBOHYD 165 165
CC CARBOHYD 266 266
CC CARBOHYD 377 378
CC ACT_SITE 413 AA; 4620 MW; AB65A1D31B8CA2BC CRC64;
CC SEQUENCE 413 AA; 52.3%; Score 1399.5; DB 1; Length 413;
CC Query Match
CC Best Local Similarity 66.5%; Pred. No. 2.3e-86;
CC Matches 268; Conservative 61; Mismatches 69; Indels 5; Gaps 1;
QY 101 SCVSPVKAMEDPQGDAAQKTDTSHTDQHPFNKTNLAFAFSLYROLAHSNSTNIF 160
Db 16 SCVSPVKAMEDPQGDAAQKTDTSHTDQHPFNKTNLAFAFSLYROLAHSNSTNIF 70

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QY 161 FSPVSIATATFAMLSLGTAKADTHDEILEGLNFNLTETPEAQHEGQELLRTLNQDPSOLQ 220
Db 71 FSPVSIATATFAMLSLGTAKADTHDEILEGLNFNLTETPEAQHEGQELLRTLNQDPSOLQ 130
QY 221 LITGNGLFTSEGLKLYDKFLEDEKLYHSEAFVFGDTEEAARKOLNDVKEGTQCKIVD 280
Db 131 LITGNGLFTSEGLKLYDKFLEDEKLYHSEAFVFGDTEEAARKOLNDVKEGTQCKIVD 190
QY 281 LKELDRDVTALVNYIFFKGGKWKQPNNEQTRKDFHVDVETVVRVPMNRLGMFLHH 340
Db 191 LKELDRDVTALVNYIFFKGGKWKQPNNEQTRKDFHVDVETVVRVPMNRLGMFLHH 250
QY 341 CKKLSSWLLMKYLGKATAIFFLPDEGKQLHLENELTHDIITKFLNEDRRSASLHLPKL 400
Db 251 CSTLASWQLMDYLGKATAIFFLPDEGKQLHLENELTHDIITKFLNEDRRSASLHLPKL 310
QY 401 SITGTYDLKSVLGQGITKVFSGNADLSGVTEAPLKLKAVHKAVLTIDEKGTAAAGM 460
Db 311 SISGTYDLKSVLGQGITKVFSGNADLSGVTEAPLKLKAVHKAVLTIDEKGTAAAGM 370
QY 461 FLEAIPMSIPPEVKFKPFVFLMEQNTKSPLEFMGVNPTOK 503
Db 371 VLGNIRSLRYEIVDRPFLVVIYEHHTKSPLEFMGVNPTOK 413

RESULT 11
ALMS_TAMSI STANDARD; PRT; 413 AA.
ID ALMS_TAMSI STANDARD; PRT; 413 AA.
AC O54760;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Alpha-1-antitrypsin-like protein CM55-MS precursor.
OS Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Tamias.
OX NCBI_TaxID=64680;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98094263; PubMed=9434174;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RA "Expression of multiple alphas-1-antitrypsin-like genes in hibernating
RT species of the squirrel family."
RL Gene 204:127-132(1997).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
CC ANTI-TRYPSIN.
CC
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CC
CC EMBL; AB000547; BAA24417.1; -.
CC HSP; P01009; 1QLP.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Signal.
CC SIGNAL 1 24
CC CHAIN 25 413
CC MOD_RES 65 65
CC CARBOHYD 102 102
CC CARBOHYD 165 165
CC ACT_SITE 413 AA; 4620 MW; AB65A1D31B8CA2BC CRC64;
CC SEQUENCE 413 AA; 52.3%; Score 1399.5; DB 1; Length 413;
CC Query Match
CC Best Local Similarity 66.5%; Pred. No. 2.3e-86;
CC Matches 268; Conservative 61; Mismatches 69; Indels 5; Gaps 1;
QY 101 SCVSPVKAMEDPQGDAAQKTDTSHTDQHPFNKTNLAFAFSLYROLAHSNSTNIF 160
Db 16 SCVSPVKAMEDPQGDAAQKTDTSHTDQHPFNKTNLAFAFSLYROLAHSNSTNIF 70

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FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ ACT_SITE 378 REACTIVE BOND (BY SIMILARITY).
 SEQUENCE 413 AA; 45952 MW; 430374CA26EBAF08 CRC64;

Query Match
 Best Local Similarity 51.9%; Score 1387.5; DB 1; Length 413;
 Matches 270; Conservative 55; Mismatches 73; Indels 5; Gaps 1;

QY 101 SCVSPVKAMEDPQGDAAQKTDTSHDDQHPFNKTPNLAFAFSLYRQLAHOSNSTNIF 160
 DB 16 SCGLPGSLAQD-----AQETASQDQHPASHRIAPLAEFALSRYLVAROSNTNIF 70

QY 161 FSPVSIATAFAMLSGKADTHDEILGNLNLTEIPEAQIHGEGFQELLRTLNQPSOLQ 220
 DB 71 FSPVSIATAFAMLSGKADTHDEILGNLNLTEIPEAQIHGEGFQELLRTLNQPSOLQ 130

QY 221 LTTGNGFLSEGLKLVDFLEKLVKLYHSEAFVNFQDTEEDFHVQVTVKVPMMKRLGMSNIH 280
 DB 131 LTTGNGFLSEGLKLVDFLEKLVKLYHSEAFVNFQDTEEDFHVQVTVKVPMMKRLGMSNIH 190

QY 281 LVKELDRDTFALVNYIFFKQKWPPEVDFKDEEDFHVQVTVKVPMMKRLGMSNIH 340
 DB 191 LVKELDRDTFALVNYIFFKQKWPPEVDFKDEEDFHVQVTVKVPMMKRLGMSNIH 250

QY 341 CKKLSWLLMKLYGNATAFIFLDEKGLQHLNELTHDITKFLNEDRRSASLHPLK 400
 DB 251 CKKLSWLLMKLYGNATAFIFLDEKGLQHLNELTHDITKFLNEDRRSASLHPLK 310

QY 401 SITGYDLKSLVGLGKITKVFNSGADLSGVTEAPLKSKAVKAVLTIDEKTEAGAM 460
 DB 311 SITGYDLKSLVGLGKITKVFNSGADLSGVTEAPLKSKAVKAVLTIDEKTEAGAM 370

QY 461 FLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPFMGVKVNPTQK 503
 DB 371 VGGITFMSRPREKVFIDRPFVFLVIEHHTKSPFVGVKVNPTQK 413

RESULT 12
 ID AIT1_MOUSE STANDARD; PRT; 413 AA.
 AC P07758;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-1-antitrypsin 1-1 precursor (Serine protease inhibitor 1-1)
 GN (Alpha-1 protease inhibitor 1) (Alpha-1-antiprotease) (AAT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Liver;
 RX MEDLINE=92052104; PubMed=1946354;
 RA Borriello F., Krauter K.S.;
 RT "Multiple murine alpha 1-protease inhibitor genes show unusual
 evolutionary divergence";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9417-9421(1991).
 RN [2]
 RP SEQUENCE OF 211-413 FROM N.A.
 RX MEDLINE=86163765; PubMed=3007061;
 RA Krauter K.S., Citron B.A., Hsu M.T., Powell D., Darnell J.E. Jr.;
 RT "Isolation and characterization of the alpha 1-antitrypsin gene of
 mice";
 RL DNA 5:29-36(1986).
 CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS
 CC ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
 CC THROMBIN.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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 CC -----

DR EMBL; M75721; AAC28869.1; -;
 DR EMBL; M12586; AAA51624.1; -;
 DR PIR; A25495; A25495;
 DR HSP; P01009; 8API;
 DR MGD; MGI:891971; Sp11-1;
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;
 FT Multigene family.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 413 ALPHA-1-ANTITRYPSIN 1-1.
 FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).
 FT CARBOHYD 64 64 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 246 246 H -> D (IN REF. 2).
 FT CONFLICT 323 323 P -> L (IN REF. 2).
 FT CONFLICT 404 404 L -> V (IN REF. 2).
 SQ SEQUENCE 413 AA; 46002 MW; 1124B2CC356232F4 CRC64;

Query Match 50.4%; Score 1347; DB 1; Length 413;
 Best Local Similarity 62.3%; Pred. No. 7.3e-83;
 Matches 255; Conservative 72; Mismatches 72; Indels 10; Gaps 4;

QY 96 GMSCKSVSPVKAMEDPQGDAAQKTDTSHDDQHPFNKTPNLAFAFSLYRQLAHOSN 155
 DB 14 GLC---CLVPSFLAED-----VQETDTSQKQDS-PASHEIATNLGDFALSRLVHOSN 64

QY 156 STNIFSPVSIATAFAMLSGKADTHDEILGNLNLTEIPEAQIHGEGFQELLRTLNQ 215
 DB 65 STNIFSPVSIATAFAMLSGKADTHDEILGNLNLTEIPEAQIHGEGFQELLRTLNQ 124

QY 216 DSQQLTGTGNGFLSEGLKLVDFLEKLVKLYHSEAFVNFQDTEEDFHVQVTVKVPMMKRLG 275
 DB 125 DSQQLTGTGNGFLSEGLKLVDFLEKLVKLYHSEAFVNFQDTEEDFHVQVTVKVPMMKRLG 184

QY 276 GKTVDLVKELDRDTFALVNYIFFKQKWPPEVDFKDEEDFHVQVTVKVPMMKRLG 335
 DB 185 GKTVDLVKELDRDTFALVNYIFFKQKWPPEVDFKDEEDFHVQVTVKVPMMKRLG 244

QY 336 FNIOHCKLSSWLLMKLYGNATAFIFLDEKGLQHLNELTHDITKFLNEDRRSASL 395
 DB 245 LVHHCSTLSSWLLMKLYGNATAFIFLDEKGLQHLNELTHDITKFLNEDRRSASL 304

QY 396 HLPKLSITGYDLKSLVGLGKITKVFNSGADLSGVTEAPLKSKAVKAVLTIDEKGT 454
 DB 305 HLPKLSITGYDLKSLVGLGKITKVFNSGADLSGVTEAPLKSKAVKAVLTIDEKGT 364

QY 455 EAAGAMFLAIPMSIPPEVKFNKPFVFLMIEQNTKSPFMGVKVNPTQK 503
 DB 365 EAAGAMFLAIPMSIPPEVKFNKPFVFLMIEQNTKSPFMGVKVNPTQK 413

RESULT 13
 ID AIT2_MOUSE STANDARD; PRT; 413 AA.
 AC P22599; O61283;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-1-antitrypsin 1-2 precursor (Serine protease inhibitor 1-2)
 GN (Alpha-1 protease inhibitor 2) (Alpha-1-antiprotease) (AAT).
 OS Sp11-2 OR AAT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RN MEDLINE=90152670; PubMed=2303252;
 RX Sifers R.N., Ledley F.D., Reed-Fourquet L., Ledbetter D.H.,
 RA "Complete cDNA sequence and chromosomal localization of mouse alpha
 RT 1-antitrypsin";
 RT Genomics 6:100-104 (1990).
 RL [2]
 RN SEQUENCE OF 12-413 FROM N.A.
 RP STRAIN=C57BL/6; TISSUE=Liver;
 RC MEDLINE=92052104; PubMed=1946354;
 RX Borriello F., Krauter K.S.;
 RA "Multiple murine alpha 1-protease inhibitor genes show unusual
 RT evolutionary divergence";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9417-9421(1991).
 CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS
 CC ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
 CC THROMBIN.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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 CC EMBL; M25529; AAA37132.1; -;
 DR EMBL; M75716; AAC28865.1; -;
 DR HSSP; P01009; 8API.
 DR MGD; MGI:891970; Spil-2.
 DR InterPro: IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;
 DR Multigene family.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 413 ALPHA-1-ANTITRYPSIN 1-2.
 FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).
 FT CARBOHYD 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 18 L -> M (IN REF. 2).
 FT CONFLICT 203 G -> A (IN REF. 2).
 FT CONFLICT 240 T -> M (IN REF. 2).
 FT CONFLICT 252 T -> I (IN REF. 2).
 FT CONFLICT 314 E -> D (IN REF. 2).
 FT SEQUENCE 413 AA; 45914 MW; D93B7B04E9446BC CRC64;
 SQ
 Query Match 50.3%; Score 1345; DB 1; Length 413;
 Best Local Similarity 62.6%; Pred. No. 9.9e-83;
 Matches 256; Conservative 71; Mismatches 72; Indels 10; Gaps 4;
 QY 96 GMCGRSCVSPVKAMEDPGDAAQKTDTSHTDQDPTFNKLTNPNAEFAFSLYRLAHQSN 155
 DB 14 GLC---CLVPSFLAED-----VQETDTSQKQDS-PASHEIATNLGDFALSLYRLVHQSN 64
 QY 156 STNIFSPVSIATAFAMSLGKADTHDIEILEGNFNLTPEIPEAQIHGEFQELLRTINOP 215
 DB 65 TSNIFFSPVSIATAFAMSLGSKGDTHTQILEGLQFNLTQTSEADIIHKSFOHLLQTLNRP 124
 QY 216 DSQQLTGTNGFLSEGLKLVDFKLEEDVKKLYHSEAFVNFQDTEEAKKOINDYVEKGTQ 275
 DB 125 DSELQSLSTGNGFLVNDLKLVEKFEAKNHYQAEVSVNFAESEAKKVINDFVEKGTQ 184
 QY 276 GKIVDLVLDKRDQTVFALNGYILFKGKWKPKDPDENTEEAEFHVDKSTTVKVPMTLSGM 244
 DB 185 GKIVEAVKELDQTVFALNGYILFKGKWKPKDPDENTEEAEFHVDKSTTVKVPMTLSGM 244

QY 336 FNIOHCKKLLSWLLMKYLGNTAIFLPEDEGKLOHLENELHFDITITPLENEDRRSASL 395
 DB 245 LDVHHCSTLSSWLLMDYAGNASAVFLLPEDGKMOHLEQTLNKLKELISKILLRRRLVQI 304
 QY 396 HLPKLSTGTGYDLKSVLGQIGTKVFSNGADLSGVTEE-APLKLKAVHKAVLTIDEXGT 454
 DB 305 HIPRLSISGEVNLKLTSPGKITRIFNNGADLSGVTEENAPLKLKAVHKAVLTIDETGT 364
 QY 455 EAAGAMFLEAIPSPPEVKFNKPFVFLMTEQNTKSPFMGKVVNPQK 503
 DB 365 EAAATVFEAVPMSPILRDFHPFLIFEHTQSPFVGVKVDPTHK 413
 RESULT 14
 ALT3_MOUSE STANDARD; PRT; 413 AA.
 ID AC Q00896;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-1-antitrypsin 1-3 precursor (Serine protease inhibitor 1-3)
 DE (Alpha-1 protease inhibitor 3).
 GN Spil-3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Liver;
 RX MEDLINE=92052104; PubMed=1946354;
 RA Borriello F., Krauter K.S.;
 RT "Multiple murine alpha 1-protease inhibitor genes show unusual
 RL evolutionary divergence";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9417-9421(1991).
 CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS
 CC ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
 CC THROMBIN.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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 CC EMBL; M75720; AAC28868.1; -;
 DR HSSP; P01009; 9API.
 DR MGD; MGI:891969; Spil-3.
 DR InterPro: IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;
 DR Multigene family.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 413 ALPHA-1-ANTITRYPSIN 1-3.
 FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).
 FT CARBOHYD 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 413 AA; 45854 MW; 7EAD710919A1C5B CRC64;
 SQ
 Query Match 50.1%; Score 1341; DB 1; Length 413;
 Best Local Similarity 62.6%; Pred. No. 1.8e-82;
 Matches 256; Conservative 70; Mismatches 73; Indels 10; Gaps 4;
 QY 96 GMCGRSCVSPVKAMEDPGDAAQKTDTSHTDQDPTFNKLTNPNAEFAFSLYRLAHQSN 155
 DB 14 GLC---CLVPSFLAED-----VQETDTSQKQDS-PASHEIATNLGDFALSLYRLVHQSN 64

SEQUENCE OF 374-380.
MEDLINE=91035333; PubMed=2229014;
Saito A., Sinohara H.;
"Amino acid sequence at the reactive site of rabbit alpha-1-
antiproteinases."; J. Biochem. 108:80-85(1990).
-1- FUNCTION: INHIBITOR OF SERINE PROTEASES. THE PRIMARY TARGET IS
ELASTASE, BUT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
THROMBIN.
-1- SUBCELLULAR LOCATION: Extracellular.
-1- TISSUE SPECIFICITY: PLASMA.
-1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

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